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TECH CENTER 1600/2003



1600

RAW SEQUENCE LISTING

DATE: 07/14/2003

PATENT APPLICATION: US/09/701,586D

TIME: 10:28:45

Input Set : A:\701586

Output Set : N:\CRF4\07142003\I701586D.raw

See page 6.

3 <110> APPLICANT: Kock, Michael
 4 Hoeger, Thomas
 5 Kroeger, Burkhard
 6 Otterbach, Bernd
 7 Lubisch, Wilfried
 8 Lemaire, Hans-Georg
 10 <120> TITLE OF INVENTION: Poly (ADP-ribose) polymerase-gene
 12 <130> FILE REFERENCE: 0050/49100
 14 <140> CURRENT APPLICATION NUMBER: US 09/701,586D
 C--> 15 <141> CURRENT FILING DATE: 2000-11-30
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03889
 18 <151> PRIOR FILING DATE: 1999-06-04
 20 <160> NUMBER OF SEQ ID NOS: 35
 22 <170> SOFTWARE: PatentIn/WordPerfect
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1843
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (3)...(1715)
 32 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from brain tissue
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 37 Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg
 38 1 5 10 15
 40 gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95
 41 Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
 42 20 25 30
 44 gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg 143
 45 Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
 46 35 40 45
 48 aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191
 49 Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
 50 50 55 60
 52 gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
 53 Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala
 54 65 70 75
 56 cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287
 57 Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
 58 80 85 90 95
 60 tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc 335
 61 Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu

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62	100	105	110	
64	cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat	383		
65	Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp			
66	115 120 125			
68	gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa	431		
69	Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys			
70	130 135 140			
72	atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc	479		
73	Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala			
74	145 150 155			
76	aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg	527		
77	Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp			
78	160 165 170 175			
80	gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta	575		
81	Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu			
82	180 185 190			
84	cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa	623		
85	Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys			
86	195 200 205			
88	gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt	671		
89	Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu			
90	210 215 220			
92	cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa	719		
93	Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu			
94	225 230 235			
96	gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg	767		
97	Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly			
98	240 245 250 255			
100	aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag	815		
101	Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys			
102	260 265 270			
104	att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa	863		
105	Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu			
106	275 280 285			
108	gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt	911		
109	Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg			
110	290 295 300			
112	act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa	959		
113	Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln			
114	305 310 315			
116	tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa	1007		
117	Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys			
118	320 325 330 335			
120	aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac	1055		
121	Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn			
122	340 345 350			
124	cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa	1103		
125	Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys			
126	355 360 365			

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128	gtg	att	tcc	cag	tac	cta	caa	tct	acc	cat	gct	ccc	aca	cac	agc	gac	1151
129	Val	Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp	
130			370					375					380				
132	tat	acc	atg	acc	ttg	ctg	gat	ttg	ttt	gaa	gtg	gag	aag	gat	ggg	gat	1199
133	Tyr	Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu	
134		385					390					395					
136	aaa	gaa	gcc	ttc	aga	gag	gac	ctt	cat	aac	agg	atg	ctt	cta	tgg	cat	1247
137	Lys	Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	Trp	His	
138	400					405					410					415	
140	ggg	tcc	agg	atg	agt	aac	tgg	gtg	gga	atc	ttg	agc	cat	ggg	ctt	cga	1295
141	Gly	Ser	Arg	Met	Ser	Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg	
142				420						425					430		
144	att	gcc	cca	cct	gaa	gct	ccc	atc	aca	ggg	tac	atg	ttt	ggg	aaa	gga	1343
145	Ile	Ala	Pro	Pro	Glu	Ala	Pro	Ile	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly	
146			435					440					445				
148	atc	tac	ttt	gct	gac	atg	tct	tcc	aag	agt	gcc	aat	tac	tgc	ttt	gcc	1391
149	Ile	Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala	
150		450					455					460					
152	tct	cgc	cta	aag	aat	aca	gga	ctg	ctg	ctc	tta	tca	gag	gta	gct	cta	1439
153	Ser	Arg	Leu	Lys	Asn	Thr	Gly	Leu	Leu	Leu	Leu	Ser	Glu	Val	Ala	Leu	
154		465					470					475					
156	ggg	cag	tgt	aat	gaa	cta	cta	gag	gcc	aat	cct	aag	gcc	gaa	gga	ttg	1487
157	Gly	Gln	Cys	Asn	Glu	Leu	Leu	Glu	Ala	Asn	Pro	Lys	Ala	Glu	Gly	Leu	
158	480				485					490					495		
160	ctt	caa	ggg	aaa	cat	agc	acc	aag	ggg	ctg	ggc	aag	atg	gct	ccc	agt	1535
161	Leu	Gln	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Met	Ala	Pro	Ser	
162				500						505					510		
164	tct	gcc	cac	ttc	gtc	acc	ctg	aat	ggg	agt	aca	gtg	cca	tta	gga	cca	1583
165	Ser	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro	
166			515						520					525			
168	gea	agt	gac	aca	gga	att	ctg	aat	cca	gat	ggg	tat	acc	ctc	aac	tac	1631
169	Ala	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr	
170		530						535					540				
172	aat	gaa	tat	att	gta	tat	aac	ccc	aac	cag	gtc	cgt	atg	cgg	tac	ctt	1679
173	Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu	
174		545					550					555					
176	tta	aag	gtt	cag	ttt	aat	ttc	ctt	cag	ctg	tgg	tga	atgttgatat				1725
177	Leu	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp						
178	560				565					570							
180	taaataaaacc	agagatctga	tcttcaagca	agaaaataag	cagtgttgta	cttgtgaatt											1785
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186	<211>	LENGTH: 570															
187	<212>	TYPE: PRT															
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190	<400>	SEQUENCE: 2															
192	Met	Ala	Ala	Arg	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala	
193	1			5						10				15			
195	Leu	Asn	Glu	Ser	Lys	Arg	Val	Asn	Asn	Gly	Asn	Thr	Ala	Pro	Glu	Asp	

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196		20		25		30	
198	Ser Ser Pro	Ala Lys Lys Thr Arg	Arg Cys Gln Arg Gln	Glu Ser Lys			
199		35		40		45	
201	Lys Met Pro	Val Ala Gly Gly Lys	Ala Asn Lys Asp Arg	Thr Glu Asp			
202		50		55		60	
204	Lys Gln Asp	Glu Ser Val Lys	Ala Leu Leu Leu Lys	Gly Lys Ala Pro			
205	65		70		75		80
207	Val Asp Pro	Glu Cys Thr Ala Lys	Val Gly Lys Ala His	Val Tyr Cys			
208		85		90		95	
210	Glu Gly Asn	Asp Val Tyr Asp	Val Met Leu Asn Gln	Thr Asn Leu Gln			
211		100		105		110	
213	Phe Asn Asn	Asn Lys Tyr Tyr Leu	Ile Gln Leu Leu Glu	Asp Asp Ala			
214		115		120		125	
216	Gln Arg Asn	Phe Ser Val Trp Met	Arg Trp Gly Arg Val	Gly Lys Met			
217		130		135		140	
219	Gly Gln His	Ser Leu Val Ala Cys	Ser Gly Asn Leu Asn	Lys Ala Lys			
220	145		150		155		160
222	Glu Ile Phe	Gln Lys Lys Phe Leu	Asp Lys Thr Lys Asn	Asn Trp Glu			
223		165		170		175	
225	Asp Arg Glu	Lys Phe Glu Lys Val	Pro Gly Lys Tyr Asp	Met Leu Gln			
226		180		185		190	
228	Met Asp Tyr	Ala Thr Asn Thr Gln	Asp Glu Glu Glu Thr	Lys Lys Glu			
229		195		200		205	
231	Glu Ser Leu	Lys Ser Pro Leu Lys	Pro Glu Ser Gln Leu	Asp Leu Arg			
232		210		215		220	
234	Val Gln Glu	Leu Ile Lys Leu Ile	Cys Asn Val Gln Ala	Met Glu Glu			
235	225		230		235		240
237	Met Met Met	Glu Met Lys Tyr Asn	Thr Lys Lys Ala Pro	Leu Gly Lys			
238		245		250		255	
240	Leu Thr Val	Ala Gln Ile Lys Ala	Gly Tyr Gln Ser Leu	Lys Lys Ile			
241		260		265		270	
243	Glu Asp Cys	Ile Arg Ala Gly Gln	His Gly Arg Ala Leu	Met Glu Ala			
244		275		280		285	
246	Cys Asn Glu	Phe Tyr Thr Arg Ile	Pro His Asp Phe Gly	Leu Arg Thr			
247		290		295		300	
249	Pro Pro Leu	Ile Arg Thr Gln Lys	Glu Leu Ser Glu Lys	Ile Gln Leu			
250	305		310		315		320
252	Leu Glu Ala	Leu Gly Asp Ile Glu	Ile Ala Ile Lys Leu	Val Lys Thr			
253		325		330		335	
255	Glu Leu Gln	Ser Pro Glu His Pro	Leu Asp Gln His Tyr	Arg Asn Leu			
256		340		345		350	
258	His Cys Ala	Leu Arg Pro Leu Asp	His Glu Ser Tyr Glu	Phe Lys Val			
259		355		360		365	
261	Ile Ser Gln	Tyr Leu Gln Ser Thr	His Ala Pro Thr His	Ser Asp Tyr			
262		370		375		380	
264	Thr Met Thr	Leu Leu Asp Leu Phe	Glu Val Glu Lys Asp	Gly Glu Lys			
265	385		390		395		400
267	Glu Ala Phe	Arg Glu Asp Leu His	Asn Arg Met Leu Leu	Trp His Gly			
268		405		410		415	

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270 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
 271 420 425 430

273 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile

274 435 440 445

276 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser

277 450 455 460

279 Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly

280 465 470 475 480

282 Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu

283 485 490 495

285 Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser

286 500 505 510

288 Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala

289 515 520 525

291 Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn

292 530 535 540

294 Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu

295 545 550 555 560

297 Lys Val Gln Phe Asn Phe Leu Gln Leu Trp

298 565 570

301 <210> SEQ ID NO: 3

302 <211> LENGTH: 2265

303 <212> TYPE: DNA

304 <213> ORGANISM: Homo sapiens

306 <220> FEATURE:

307 <221> NAME/KEY: CDS

308 <222> LOCATION: (242)...(1843)

309 <223> OTHER INFORMATION: product is Poly ADP Ribose Polymerase; from uterus tissue

311 <400> SEQUENCE: 3

313 tgggactggt cgcctgactc ggctgcccc agcctctgct tcaccccact ggtggccaaa 60

315 tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattg ttgggaattc 120

317 tctccctaatt tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag 180

319 gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttgge 240

321 c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag 286

322 Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu

323 1 5 10 15

325 aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc tcc 334

326 Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser

327 20 25 30

329 acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc cgc 382

330 Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg

331 35 40 45

333 gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg tat 430

334 Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr

335 50 55 60

337 gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac aac 478

338 Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn

339 65 70 75

341 aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc 526

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,4,5,6,7,9,10,11
Seq#:12; Xaa Pos. 1,2,6,7,9,10,11,12,13,14,16,17,18
Seq#:13; Xaa Pos. 6,7,8,9,10,11,12,13,16,17,21,22,24,25,26,27,28,29,31,32
Seq#:13; Xaa Pos. 33,41,42,43,48
Seq#:14; Xaa Pos. 1,2,3,4,5,6,7,9,10,11,12,13,14,16,17,18,19,20,21
Seq#:15; Xaa Pos. 2,3,4,5,6,7,8,9,10,12,13,15,16,20,21,22,23,24,25,26,27,28
Seq#:15; Xaa Pos. 29,30,31,32
Seq#:16; Xaa Pos. 2,3,4,6,8,9,10,11,14,16,18,19,20,21,22,24,25,26,28
Seq#:17; Xaa Pos. 2,4,5,6,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23,24,25
Seq#:17; Xaa Pos. 26,27,33,34,35,38,39,40,41,42,43
Seq#:18; Xaa Pos. 4,8,11,12,13
Seq#:19; Xaa Pos. 2,3,4,6,7,9,13,15,16
Seq#:20; Xaa Pos. 2,3,4,6
Seq#:21; Xaa Pos. 2,3,5,6,7,8,10,11,12,14,15,16,17,18,19,20,21,22,24,26,27
Seq#:22; Xaa Pos. 2,3,4,6,7,8,10,11,12,13
Seq#:29; Xaa Pos. 2,3,4
Seq#:30; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:30; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,34,36,37
Seq#:34; Xaa Pos. 36,48,51,52,53,57,68,72,74,80,85,89,92,106,122,126,147
Seq#:34; Xaa Pos. 156,160,173,177,189,191,202,205,212,226,242,245,275,277
Seq#:34; Xaa Pos. 280,291,302,304,313,332,336,337,338,340,342,370,385,393
Seq#:34; Xaa Pos. 404,467,470,475,492,493,540,543,545,558,575

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:1432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

M:341 Repeated in SeqNo=12

L:1464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

M:341 Repeated in SeqNo=13

L:1497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0

M:341 Repeated in SeqNo=14

L:1524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

M:341 Repeated in SeqNo=15

L:1549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0

M:341 Repeated in SeqNo=16

L:1576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0

M:341 Repeated in SeqNo=17

L:1601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0

L:1620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0

L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0

L:1662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0

M:341 Repeated in SeqNo=21

L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0

L:1805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0

L:1824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0

M:341 Repeated in SeqNo=30

L:1897 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:32

M:341 Repeated in SeqNo=34
